

Curriculum Vitae of Andreas Rechtsteiner

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- EDUCATION ♦ **Ph.D.** in Systems Sciences Program, Portland State University, Portland, Oregon (research performed at Los Alamos National Laboratory).
Expected graduation: Summer 2005. Dissertation title: Multivariate analysis of gene expression data and functional information: Automated methods for Functional Genomics.
- ♦ **M.Sc.** in Systems Sciences Program, Portland State University, Fall 2000.
- ♦ **M.Sc.** in Physics, Portland State University, Spring 1996.
- ♦ **Zwischenprüfung** in Teaching Mathematics and Physics at high school level (corresponding to Bachelor Degree), Summer 1993.
- ♦ **Vordiplom** in Physics (corresponding to B.Sc. in Physics), Spring 1993.
- RESEARCH ♦ **Information Retrieval and Integration for Functional Genomics**
EXPERIENCE Mining of literature for gene expression cluster validation and functional annotation and protein
IN BIOINFOR- family classification. Information Retrieval techniques like Latent Semantic Analysis were used to
MATICS analyze the associations of genes and proteins with keywords in the literature.
- ♦ **Multivariate Analysis of Gene Expression Microarray Data**
A method was developed that identifies significantly expressed genes in a time series experiment based on the correlation of the expression vectors with a 2-dimensional expression subspace. Singular Value Decomposition has been used to identify such subspaces.
- FURTHER ♦ **Hidden Markov Models and Dynamical Systems Modeling**
RESEARCH Novel Hidden Markov Models with several different output and state transition models were de-
EXPERIENCE veloped. Different dynamical processes, among them the changes in global pressure patterns, were
modeled. (Work was performed within a NASA grant and for M.Sc. in SySc with Prof. Andrew Fraser.)
- ♦ **Evolutionary Simulations**
Work on quantification of adaptive change in different evolutionary models, among them John Holland's Echo model and models of *neutral evolution* (i.e. models of random genetic drift without causing changes in phenotype fitness). (Work with Prof. Mark Bedau at Reed College, Portland, OR)
- ♦ **Cellular Automata**
Fractal dimensions in cellular automata. (Work for M.Sc. in Physics, with Prof. Jack Semura at PSU)
- COMPUTER ♦ **Operating Systems and Platforms**
AND PRO- Unix (Linux, Solaris, IRIX) on Intel, SUN and SGI platforms (SGI Origin 2000 cluster at Los
GRAMMING Alamos National Laboratory).
SKILLS Experience with Windows and Macintosh platforms.
- ♦ **Programming Languages and Tools**
C, Perl, Fortran 90, HTML, Visual Basic.

◇ **High-Performance Computing**

Experience with OpenMP and MPI through parallel implementation of Monte Carlo plasma simulation code on SGI Origin 2000 system at Los Alamos National Laboratory.

◇ **Applications**

GNU tools, GNU Emacs, L^AT_EX, R, SPlus, Matlab/Octave, Gnuplot, Maple, and others.

◇ **Biological Databases**

Experience with MEDLINE, MeSH, SwissProt, GenBank, PFAM, SCOP and others.

PUBLICATIONS
IN JOURNALS,
BOOKS AND
CONFER-
ENCES

Challacombe, J., A. Rechtsteiner, R. Gottardo, L.M. Rocha, E.P. Brown, T. Shenk, M. Altherr, T. Brettin. Evaluation of the host transcriptional response to human cytomegalovirus infection. *Physiol. Genomics* (April 6, 2004). 10.1152/physiolgenomics.00155.2003 (in press).

Rocha, L.M. and Rechtsteiner, A. Review of the book “Bioinformatics for Geneticists”, Michael R. Barnes and Ian C. Gray (Eds). *Clinical Chemistry*. 2004 (in press).

Karin Verspoor, Judith Cohn, Cliff Joslyn, Sue Mniszewski, Andreas Rechtsteiner, Luis M. Rocha, Tiago Simas. Protein Annotation as Term Categorization in the Gene Ontology using Word Proximity Networks. *BMC Bioinformatics*. 2004 (in press).

Rechtsteiner, A. and L.M. Rocha. MeSH Key Terms for Validation and Annotation of Gene Expression Clusters. *Currents in Computational Molecular Biology*. Proceedings of the *Eight Annual International Conference on Research in Computational Molecular Biology* (RECOMB 2004), San Diego, CA, March 2004. A. Gramada and Philip E. Bourne (Eds). pp. 212-213.

Rechtsteiner, A, Gottardo, R, Wall, ME, Rocha, LM. A new SVD based algorithm for detection of interestingly and significantly expressed genes in gene expression data. *Currents in Computational Molecular Biology*. Proceedings of the International Conference on Research in Computational Molecular Biology (RECOMB 2003), Berlin, Germany, April 2003. R. Spang, P. Beziat and M. Vingron (Eds). pp. 275-276

Wall ME, Rechtsteiner A, and Rocha L. Singular Value Decomposition and Principal Component Analysis. In: *A Practical Approach to Microarray Data Analysis*. Berrar D, Dubitzky W and Granzow M. (Eds). pp. 91-109. Kluwer Academic Publishers. 2003.

Rechtsteiner, Andreas and Andrew M. Fraser. Hidden States for Modeling Interactions between disparate Spatiotemporal Scales. Proceedings of the *International Conference on Complex Systems* (ICCS), 2000.

Rechtsteiner, Andreas and Mark A. Bedau. A generic neutral model for quantitative comparison of genotypic evolutionary activity. In D. Floreano, J.-D. Nicoud, F. Mondada, eds., *Fifth European Conference on Artificial Life* (pp. 109-118). Heidelberg: Springer-Verlag, 1999.

Rechtsteiner, Andreas and Mark A. Bedau. A generic neutral model for measuring excess evolutionary activity of genotypes. In W. Banzhaf, J. Daida, A. E. Eiben, M. H. Garzon, V. Honavar, M. Jakiela, and R. E. Smith, eds., GECCO-99: Proceedings of the *Genetic and Evolutionary Computation Conference*, Orlando, Florida USA, 1999.

WORKSHOP
AND POSTER
PRESENTA-
TIONS

Rechtsteiner, A. and L.M. Rocha. Use of Medline’s Mesh Terms for Automated Functional Annotation. Presentation at *ISCB Rocky Mountain Regional Bioinformatics Meeting*, Aspen, CO, December 2003.

Rocha, Luis M. and Rechtsteiner, Andreas. Fast Cheap and Synthetic Oracle (FACSO): Proximity Measures to capture Expert Knowledge in the Bibliome, LAUR 03-0562, *Pacific Symposium on Biocomputing*, 2003.

Rechtsteiner, Andreas. Singular Value Decomposition for Gene Expression Data Analysis. Poster at the *Program in Mathematics and Molecular Biology (PMMB) workshop*, Santa Fe, NM, 2002.

Rechtsteiner, Andreas. Seasonal Hidden Markov Models. Proceedings of the *SIAM Dynamical Systems Conference*, Snowbird, UT, 2001.

RESEARCH
POSITIONS

9/1998 - 6/2000: Graduate Research Assistant in the PSU Systems Sciences Program. Research in the fields of Dynamical Systems Modeling with Hidden Markov Models and Evolutionary Simulations.

7/2000 - 11/2000: Graduate Research Assistant in group X-4, Los Alamos National Laboratory. Development of parallel Monte Carlo plasma simulation code.

11/2000 - 11/2001: Graduate Research Assistant in Bioscience Division at Los Alamos National Laboratory. Work on gene expression data normalization and analysis.

11/2001 - currently: Graduate Research Assistant in the Modeling, Algorithms and Informatics Group (CCS-3) at Los Alamos National Laboratory. Research on Spectral Techniques for Gene Expression Analysis and development of Information Retrieval techniques for Bioinformatics applications.